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OM nucleic - nuc	nucleic search, using sw model
Run on:	April 29, 2003, 16:34:19 ; Search time 6488 Seconds (without alignments) 16982.618 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-715-876-7 3786 1 atgottcaacaatttacatttgtcottgttcatttagtga 3786
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
number of	hits satisfying chosen parameters: 4109280
Minimum DB seq l Maximum DB seq l	length: 0 length: 200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmb1:*
	1: gb_ba:*
,	2: gb_htg:* 3: gb_in:*
	5: gb_ov:*
	8: gb_pl:*
	3. gb_pr:*
	11: gb_sts:*
	12: gb_sy:*
	14: gb_vi:*
	15: em_ba:* 16: em_tin:*
	17: em_hum:*
	18: em_in:* 10: em_in:*
	21: em_or:* 22: em_or:*
	25: em_p1:* 26: em_ro:*
	28: em_un:* 20: om ::i:*
•	32: em_nrg_orner:* 33: em_htq_mus:*
	-
	33: em_ntg_rod:* 36: em_htg_mam:*
	39: em_htgo_hum:*
	40: em_htgo_mus:* 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a 9b\_pr:\*
9b\_pr:\*
9b\_pr:\*
9b\_pr:\*
9b\_yr:\*
9b\_yr:\*
9b\_pr:\*
em\_bu:\*
em\_fun:\*
em\_hu:\*
em\_nu:\*
em\_nu:\*
em\_pr:\*
em\_pr

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB 1D  3786 100.0  3786 8 YEACH LENGTH B  1884 100.0  3786 8 YEACH LENGTH B  1786 100.0  3786 8 YEACH LENGTH B  1788 100.0  3	Score   March   Length   DB   DB			di			SUMMARIES		
1844   485   3360   8   KSAALSI   100.0   3786   8   KSAALSI   100.0   3786   8   KSAALSI   100.0   3786   8   KSAALSI   100.0   3786   8   AF023429   A	3786 100.0 3786 8 YSAALS1 125902 Candid 1783 4 48.5 3360 8 CAUB7956 AP051313 Candid 1786 4 5.3 360 9 AF051313 Candid 1783 4 48.5 3360 9 AF051313 Candid 1783 8 AF052429 AF052429 AF052429 Candid 1783 18.3 8 AF068866 Candid 1785 2 1071 6 AF074076 AF074076 Seq. 1785 2 1071 6 AF074076 AF074076 AF074076 Seq. 1785 2 1071 6 AF074076 AF074076 AF074076 Seq. 1785 2 1071 6 AF075293 AF074076 Seq. 1785 2 1 1404 8 CANLESS1 AF074076 AF074	sul No	Scor	Query Match	Length	Ω	ID		Description
1834.4   48.5   3360   8   APO51313   APO5	1834   48   5   3360   8   APPG1313   Candid Cand	1	37	100.0	3786	ı	YSAALS	1 1 1 1 1 1 1	L25902 Candida
1708   6 45.1   438   8 AF051313   AF05131	150   150	8	834	8	36	œ	795		dida
1322.8 4 70.3 9 AF272027 AF272027 AF272027 Cand 198.8 31.4 3813 8 AF068866 AF068866 AF068866 Cand 198.8 31.4 3813 8 AF068866 Cand 198.8 31.4 3813 8 AF068866 Cand 1069.4 28.2 1071 6 155422 AF024882 Cand 1065.2 2.1 1071 6 155423 AF206886 Cand 874.8 23.3 432.8 AF2075293 AF2076894 AF2075293 Cand 874.8 22.3 1407 8 CANALS4231 AF2229999 Cand 875.4 21.3 1407 8 CANALS4231 AF2229999 Cand 875.4 21.3 1407 8 CANALS4231 AF2229999 Cand 875.4 21.3 1407 8 AF2075294 AF2075294 Cand 876.2 21.3 1407 8 AF2075294 Cand 876.2 21.3 1407 8 AF2075294 Cand 876.2 21.3 1407 8 AF2075294 AF207529 Cand 876.2 21.3 1407 8 AF2075294 AF2075294 Cand 876.2 21.3 1407 8 AF2075294 AF2075294 AF2075294 Cand 876.2 21.3 140.8 AF2075294 AF2075294 AF2075294 Cand 876.2 21.3 140.8 AF2075294 AF207686 Cand 876.2 21.3 140.8 AF2075294 AF207686 Cand 876.2 21.3 140.8 AF207689 A	1352.8 4 70.3 4 70.9 8 AF0.720.7 AF0.254.29 Cancel 1932.8 3 6.8 4 72.3 8 AF0.720.7 Cancel 1969.4 28.2 10.71 6 1665.3 AF0.6866 Cancel 1069.4 28.2 10.71 6 1665.3 AF0.6866 Cancel 1069.4 28.2 10.71 6 1665.3 AF0.245.9 Cancel 1069.4 28.2 10.71 6 1665.3 AF0.245.9 Cancel 1069.4 28.2 10.71 6 1665.3 AF0.245.9 Cancel 20.5 8 23.9 43.2 AF0.164.9 Cancel 20.3 140.4 BAF0.165.9 AF0.165.9 AF0.166.9 AF	m <del>-</del>	708	o	ສະ	<b>x</b>	5131		andid
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/db_xref="taxon:5476"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3786; Conservative 0; Mismatches
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/protein_id="AAC41649.2"
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TCTCAATCATATGCAACCACTACCATTACCGCTCCACCTGGTGAAACTGATACCGTT 
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TYGDVQIDCSXHVGTRKGLANDWYPYSSESFSYTKTCSSAGTGFFTYKRVPAGYRPFV
DAY ISATDVNSYTLSANBYTGAGGYWQRAPFTLRWFGYRSDAGSNGIVIVATTRPY
TDSTTAVTTLPFDPNRDKTKTIEILKPIPTTITTSVUGVTTSYSTKTAPIGETATVI
YDTPHTYTYDKSWFGTITSTTTHYNFDSLIOTVIVQVPSRRTYTFERWSGSFAT
TTTTTGPPGRMTDYLIREPRHITVTTTEWSESYTTTSTFTAPPGGTDSVIIKEPPNP
TVTTTEYWSESYTTTSTFTAPPGGTDSVIIKEPPNP
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EFMTFSTLTCTVSNTLTPSIKALGTVTLPPLAFNVGGTGSSVDLEDSKCFTAGTNTVTF
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                                        3720
                                                                                 Hoyer, L. L.
Direct Submission
Submitted (30-JAN-1997) Veterinary Pathobiology, University of Submitted (300-JAN-1997) Veterinary Pathobiology, University of Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
          TCTATTATCCAACATTCTACTTGGTTGTACGGTTTGATCACATTATTGTCCTTGTTCATT
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/db_xref="G1:3273415"
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/gene="ALS3"
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                                        Score 1834.4;
Pred. No. 0;
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Matches 2393; Conservative
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GGATCTAACGGTATTGTTGTGGCTACTACCAGACAGTTACAGACAG	ACTGATTCAATTGACACGGTGGTGGTACAAGTTCCACTGCCAAATCCAACTGTTAGTACT ACTGACTCAATAGACACTGTCATTGTACAAGTTCCACTGCCAAATCCAACTGTTAGTACT ACTGACTCAATAGGACACTGTCATTGTACAAGTTCCACTGCCAACCCAACTGTTACTACC ACTGAATATTGGTCTCAGTCTTTGCTACAACTCACACACTGTTACTGGTGTTACTGGTCTTAGTTTGCTACACCACCACCACCACTACTGGACACCAGGACACACAC	ATTATCAAGAACCACACACTACATACAACGAATTGGTCATTCAT	ACTGTCACTACTACTGAATACTTATACCACCACTACCACTGCAACTCACTACTACTACTACTACTACTACTACTACTACTA
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                                                                                                                                  surface protein (ALS8) gene,
                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

(bases 1 to 4383)
Leng, P., Lee, P.R., Wishart, J.A., Wu, H. and Brown, A.J.P.
Sequence of the hypha-specific, agglutinin-like cell surface protein, ALS8 from Candida albicans
                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 4383)
Leng,P., Lee,P.R., Mishart,J.A., Wu,H. and Brown,A.J.P.
Direct Submission
Submitted (29-UUL-1999) Molecular and Cell Biology, University on Aberdeen, Institute of Medical Sciences, Foresterhill, Aberdeen AB25 22D, UK
On Aug 1, 2000 this sequence version replaced gi:4105850.
Location/Qualifiers
                    3172 AGTACTTTAGCATCTGCAAGTGAAGAAGACAACAAAAAGCGGTTCTCATGAATCAGCAT 3229
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'note="minor form"
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/protein_id="AAD02580.1"
/db_xref="GI:4105851"
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/note="minor form"
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Candida albicans agglutinin-like cell
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/db_xref="ATCC:10261"
/db_xref="taxon:5476"
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/bound_moiety="Efglp"
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/gene="ALS8"
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NDGTTSISATVDFRKSTVASSBILLDSRILDFSLSQAYSLFLPPBCANGYTSGTNGFST
AGGATIDCSTVHVGISNGLNDWNYPISSESFSYTKTCTSTSVLVTYGNVPAGYRRFV
DAYYSATRYSSYAMYTNIYACVGAASVDDSFTHTWSGYSNSQAGSNGITIVVTTRTV
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Candida albicans agglutinin-like protein mRNA, partial cds.
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Chen,X. and Chen,J.-Y.
Direct Submission
Submitted (24-MAY-2000) Shanghai Institute
Yang Road 320, Shanghai 200031, China
Location/Qualifiers
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∕organism≕"Candida albicans"
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[ Obases I to 4723]

Gaur, N. K. and Klotz, S. A.

Expression, cloning, and characterization of a Candida albicans gene, ALA1, that confers adherence properties upon Saccharomyces cerevisiae for extracellular matrix proteins

Infect. Immun. 65 (12), 5289-5294 (1997)
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/function="cell adhesion protein"
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Gaur, N.K. and Klotz, S.A.
Direct Submission
Submitted (15-SEP-1997) Research Service,
Linwood Blvd., Kansas City, MO 64128, USA
Location/Qualifiers
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327. .4586
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/organism="Candida
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/gene="ALA1"
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TTIITSKPGTDSYINREPHNPTVTTTEWSESFATTETITSKPBGTDSVIVREPHNP
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                                                 /translation="MIQQFTLLFLYLSFATAKAITGIFNSIDSLTWSNAGNYAFKGPG
YPTWNAVLGWSLDGTSANPGDTFILNMPCVFKFTASQKSVDLTADGVKYATCQFYSGE
                                                                                                 NDGSKKLSIAVNFEKSTVDQSGYLTTSRFMPSLNKIATLYVAPQCENGYTSGTMGFST
SYGDVAIDCSNVHIGISKGVNDWNHPVTSESFSYTKSCSSFGISITYQNVPAGYRPFI
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QQVATSSYNQPLITTYAGSSSATKHPSWLLKFISVALFFFL"
1013 c 803 g 1466 t
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Pred. No. 1.1e-241;
0; Mismatches 362;
/product="agglutinin-like adhesin"
/protein_id="AAB8883.1"
/db_xref="GI:2522219"
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Best Local Similarity 81.6%;
Matches 1610; Conservative
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          GGTGACGTTGCTATTGATTGCTCAAATATTCATATTGGTATCACAAAAGGATTAAATGAT
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/translation="MIQQFTLLFLYLSFATAKAITG1FNSIDSLTWSNAGNYAFKGPG
YPTWNAVLGWSLDGTSANPGDTFILNMPCVFKFTASQKSVDLTADGVKYATCQFYSGE
EFTTFSTLTCTVNDALKSSIKAFGTVTLP1AFNVGGTGSSTDLEDSKCFTAGINTVTF
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Pathobiology, University of
S. Lincoln Avenue, Urbana,
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                                                                             ACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATTATCAGAGAACCACCAAACCAC
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Candida.
Saccharomycetales; Candida.
1 (bases 1 to 3813)
Hoyer, L.L. and Hecht, J.E.
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/protein_id="AAD32849.1"
/db_xref="GI:4903269"
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3 (bases I to 3813)
Hoyer,L.L., Ho,M. and Hecht,J.E.
Direct Submission
Submitted (28-MAY-1998) Veterinary
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Candida albicans agglutinin-like
allele, complete cds.
AF068866 IG:4903268
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Hoyer, L.L., Ho, M. and Hecht, J.E.
The ALS5, ALS6 and ALS7 genes of
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/chromosome="3"
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/gene="ALS5"
/allele="ALS5-1"
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Yeast 18 (1), 49-60 (2001)
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/transl_table=12
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ö Gaps 9 9 ATGCTTCAACAATTTACATTGTTATTCCTATATTTGTCAATTGCAAGTGCAAAGACAATC 3813; .; 0 Length Indels 8; Score 1188.8; DB 8; Pred. No. 7.9e-205; 0; Mismatches 382; 31.4%; larity 78.8%; Conservative Query Match Best Local Similarity Matches 1418; Conserv ò

120 ACTGGTATTTTCAATAGTATTGACTCATTAACTTGGTCCAATGCTGGCAATTACGCTTTC ACTGGTGTTTTTGATAGTTTTAATTCATTAACTTGGTCCAATGCTGCTAATTATGCTTTC 61 61 g ò 셤

240 240 180 180 AAAGGGCCAGGATACCCAACTTGGAATGCTGTTTTGGGTTGGTCCTTAGATGGTACCAGT 121 121 181 181 Q õ g Q ò

360 360 420 TCCATTAAGGCATTTGGTACAGTTACTTTACCAATTGCATTCAATGTTGGTGGAACAGGT 301 361 ð g ò

420. 480 480 TCCATTAAGGCATTTGGTACAGTTACTTTTACCAATTGCATTCAATGTTGGTGGAACAGGT TCATCAACTGATTTGGAAGATTCTAAATGTTTTACTGCTGGTACCAATACAGTCACATTT 361 421 121 g õ q

**AATGATGGTGATAAAGATATCTCAATTGATGTTGAGTTTGAAAAGTCAACCGTTGATCCA AATGATGGCAGTAAAAAGCTCTCAATTGCTGTTAATTTTTGAAAAGTCAACAGTTGATCGA** 481 181

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GTGGCACCACAATGTGAAAATGGTTACACATCTGGTACAATGGGGTTCTCCAGTAGTAAC 541 601 g ò

AGTGCATATTTGTATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTCACAACTCTTTTT

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720 GGTGACGTTGCTATTGATTGCTCAAATATTCATATTGGTATCACAAAAGGATTAAATGAT 661 õ

1080 1260 1020 1200 1260 1380 GCTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAA 1620 TCACAATCCTTTGCTACTACTACTGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA 1500 AGTGAGTTATCTACATTTTCTAGTTCTGAGAGCTACTCGTCAAGTATCTCTGATACCACA 1800 840 960 960 840 900 720 TCTGCTACAGATGTTAACCAATATACTTTAGCATATACCAATGATTATACTTGTGCTGGC GATTATTGGCAACATGCACCTTTCACTTTAAAATGGACTGGATATAAGAATAGTGATGCC GTCACTACTTTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATCGAAATTTTGCAA CCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGGACTACTTCCTATCTGAACT ACTGATTCAATTGACACAGTGGTGGTACAAGTTCCACTGCCAAATCCAACTGTTAGTACT ACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGT ACCGATACTGTGATTATCAGAGGCCACCAAACCATACTGTCACTACTGAATATTGG ATTATCAGAGAACCACCAAATCCAACTGTCACTACAACCGAGTATTGGTCTCAATCCTTT CCTCCAAACCCAACTGTCACCACCACCACTGAATATTGGTCCCAATCTTACGCAACCACAACT GGATTGTCATCAAGTTCAGATATACCATTAAGTTCAGACATGCCATCATCGAGCTCAACT GGGTTAACATCTAGTGAGTCGTCTACTGTCTCAAGTTATGATAGCGATTCATCAAGTAGT ACTGTCACTACTACTGAATACTGGTCACAATCATATGCCACCACTACCACTGTAACTGCA GGGGATGTTGCTATTGACTGTTCAAATGTACATATTGGTATTTCAAAAGGAGTAAATGAT TGGAATTATCCGGTTTCATCTGAATCATTTAGTTACACTAAAACTTGTACATCTAATGGA ATTCAGATTAAATATCAAAATGTACCTGCTGGTTATCGTCCATTTATTGATGCTTATATT AGTCGTCTGCAAAGTAAACCTTTCACTTTAAGATGGACTGGATACAAGAATAGTGATGCC 1741 901 901 1021 1021 1081 1141 1141 1201 1261 1381 1381 1441 1441 1501 1561 1561 1621 1621 1681 781 841 1081 1201 1321 1321 1501 721 781 961 961 721 1261 αq qq g Op ò g q δ qq Ω qq ογ Db Qy Dp Oy Dp δý QQ δ Db Qy Db Oy Db oy Oy qq ò q δ òγ οý οχ ò

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Pred. No. 3.8e-183;
); Mismatches 1;
                                                                                          Unclassified.

1 (bases 1 to 1071).

Conserved yeast nucleic acid sequences Patent: US 5817466-A 1 06-OCT-1998;
                         AR044076 1071 bp
Sequence 1 from patent US 5817466.
AR044076 -AR044076.1 GI:5965541
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                                                                                                                2140 GATACCGTTCTTATCAGAGAGCCACCAAACCATACTGTCACTACTACTGAATACTGGTCT
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Pred. No. 3.8e-183;
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Hoyer, L.L., Livi, G.P., and Shatzman, A.R.
Conserved yeast nucleic acid sequences
Patent: US 5668283-A 1 16-SEP-1997;
Location/Qualifiers
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Best Local Similarity 99:9%;
Matches 1070; Conservative
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/note="agglutinin-like
/allele="ALS2-2"
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/transl_table=12
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/note="first of
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Best Local Similarity 83.2%;
Matches 1170; Conservative C
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/gene="ALS2"
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protein (ALS2) gene, 5' partial
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Candida albicans

Candida albicans

Eukaryota; Fungil. Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1404)

Hoyer, L. L., Payne, T. L. and Hecht, J. E.

Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface

J. Bacteriol. 180 (20), 5334-5343 (1998)
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Best Local Similarity 82.7%;
Matches 1163; Conservative
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1404)

Hoyer, L.L., Payne, T.L. and Hecht, J.E.

Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface

J. Bacteriol. 180 (20), 5334-5343 (1998)
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/note="first of multiple copies of imperfect 108
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Submitted (11-SEP-1997) Veterinary Pathobiology, Univers
Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
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/product="agglutinin-like protein"
/protein_id="AAC64235.1"
/db_xref="GI:3598670"
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Pred. No. 9.8e-172;
0; Mismatches 240;
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4332 bp DNA linear PLN 03-AUG-2000 strain 1161 agglutinin-like protein 6 (ALS6) gene,
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Direct Submission
Submitted (30-JUN-1998) Veterinary Pathobiology, University (
Submitted (30-JUN-1998) Veterinary Pathobiology, University (
Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
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/protein_id="AAD42033.1"
/db_xref="G1:5326752"
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Hoyer, L. L. and Hecht, J. E.
The ALS6 and ALS7 genes of Candida albicans Yeast 16 (9), 847-855 (2000)
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0; Mismatches 627;
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/strain="1161"
/db_xref="taxon:5476"
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Hayer, L. L. and Hecht, J.E.
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GMSPPIPSSEGRSSIPWSSSNESSESSESSGST
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VGELSALPSLPGKISHLPSSLSETSIGMTKSANLSPQFFSTSVDSALSYWASGSSSSAD
HQSSATCDVSESSVEGNLSAMAPGMSNSDDGLSEDTRSSSVAGKEEIELTSTNSVGEI
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SNDDDFEIDCSSIHVGITNEINDWSMPVSSVPFDHTIRCTSRALYIEFKTIPAGYRPF
VDAIVQIPTTEPFFVKYTNEFACVNGIYTSIPFTSFFSQPILYDEALAIGADLVRTTS
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VFIDVPQHTATTLTTWQESSTATTTYFDDIDLVDTVIVKIPYPNPTIITTQFWSGKY
LTTETHKEPPLGTDSVIIKEPHNPTVTTTEFWSESFATTETIINYPEGTDSVIVREPH
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VSKQVSTTVTEQYDTSTYTPASLLVSDNSGSVSKYSLMMMAFYMLFGLF"
1309. .2484
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STLTANAQLEWALDGTIASPGDIFTLVMPCVYKFMTYETSVQLTANSIAYATCDFDAG
EDTKSFSSLKCTVTDELTEDTSVFGSVILPIAFNVGGSGSKSTITDSKCFSSGYNTVT
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GPEGTDSVIVREPHNPTVTTTEFWSESFATTET ITNGPEGTDSVIVREPHNPTVTTTE
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                                                                                                                                             Direct Submission
Submitted (03-NOV-1999) Veterinary Pathobiology, University
Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
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1309. .1425
/gene="ALS7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="agglutinin-like protein Als7p"
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/protein_id="AAF98068.1"
/db_xref="G1:9754771"
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3292, .5511
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/db_xref="taxon:5476"
/chromosome="3"
Yeast 16 (9), 847-855 (2000)
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/codon_start=1
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/gene="ALS7"
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Hoyer, L.L.
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                                                                                                  Length 6897;
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Pred. No. 3.9e-148;
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/gene="ALS7"
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ATTCCAACCACTACCATCACATTCATATGTTGGTGACTACTTCCTATCTGACTAAG 1143
                                                                                                          ACTGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCACA 1203
                                                                                                                                                         AAAGCCACCATTGGTGACACACAGCTACTGTTTTCATTGATGTTCCACAACATCAACAGCTACT 1209
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                                              ACTACTTTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATCGAAATTTTGCAACCT
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DAYISATRVSSYTMQYTNIYACVGAASVDDSFTHTWRGYSNSQGGSNGITIVVTTRTV
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
I (bases 1 to 1407)
Hoyer, L.L., Payne, T.L. and Hecht, J.E.
Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface
J. Bacteriol. 180 (20), 5334-5343 (1998)
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of
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Direct Submission
Submitted (11-SEP-1997) Veterinary Pathobiology, University
Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
                                                                                                                                                                                                CCAAACCATACTGTCACTACTGCATACTGGTCTCAATCATATGCTACAACCACCACT
                                                                                                                                                                                                                                                                          GTTACTACTACTGAATATTGGTCACAATCATTTGCCACAACCACCACGGTTACTGCTCCT
                                                       ACAACCACCACTGTTACTGCACCACCTGGTGAAACCGGTACCGTTCTTATCAGAGAGCCA
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/allele="ALS4-1"
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/strain="1161"
/db_xref="taxon:5476"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                               CCAGGTGGTACTGACACTGTGATTATCTATGAA 2376
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/transl_table=12
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AF024584.1 GI:3598677
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                                                                                           Length 1407;
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                                                                                         Score 842.8; DB 8;
Pred. No. 2.8e-142;
0; Mismatches 352;
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nilarity 75.0%;
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CANALS42S1 1407 bp DNA linear PLN 16-OCT-1998 Candida albicans agglutinin-like protein (ALS4) gene, 5' partial
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1 (bases 1 to 1407)
Hoyer, L. L., Payne, T. L. and Hecht, J. E.
Identification of Candida albicans ALS2 and ALS4 and localization of als proteins to the fungal cell surface
J. Bacteriol. 180 (20), 5334-5343 (1998)
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                                                                                              Direct Submission
Submitted (11-SEP-1997) Veterinary Pathobiology, Univers
Illinois, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
Location/Qualifiers
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/allele="ALS4-2"

    .1407
    /organism="Candida albicans"

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/product="agglutinin-like protein"
/db xref="di="AAC64241.1"
/db xref="di="A8C64241.1"
/db xref="di="398686"
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/translation="MLLQFLLLSLCVSVATAKVITTGVFNSFNSLTWANSYRTRAPRAPACNASAGOTFTLDMPGVFFFTITTDGYISLDVADGRFYATGNUNASE
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NDGDTSISTTVDFEKSTVASSDRILLSRILDSRILDSLCANSYSCTMGFST
AGTATIOESTYMYTTNYADNFAMGTYTTPSSEPSVAGSTKTCTSTSTVTTRFY
TDSTTAVTTLPFNSDTDKTKTIEILQPIPTTITTSYVGVTTSYSTKTAPIGETATVI
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/note="first of multiple copies of 108bp imperfect repeat"
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Pred. No. 4e-141;
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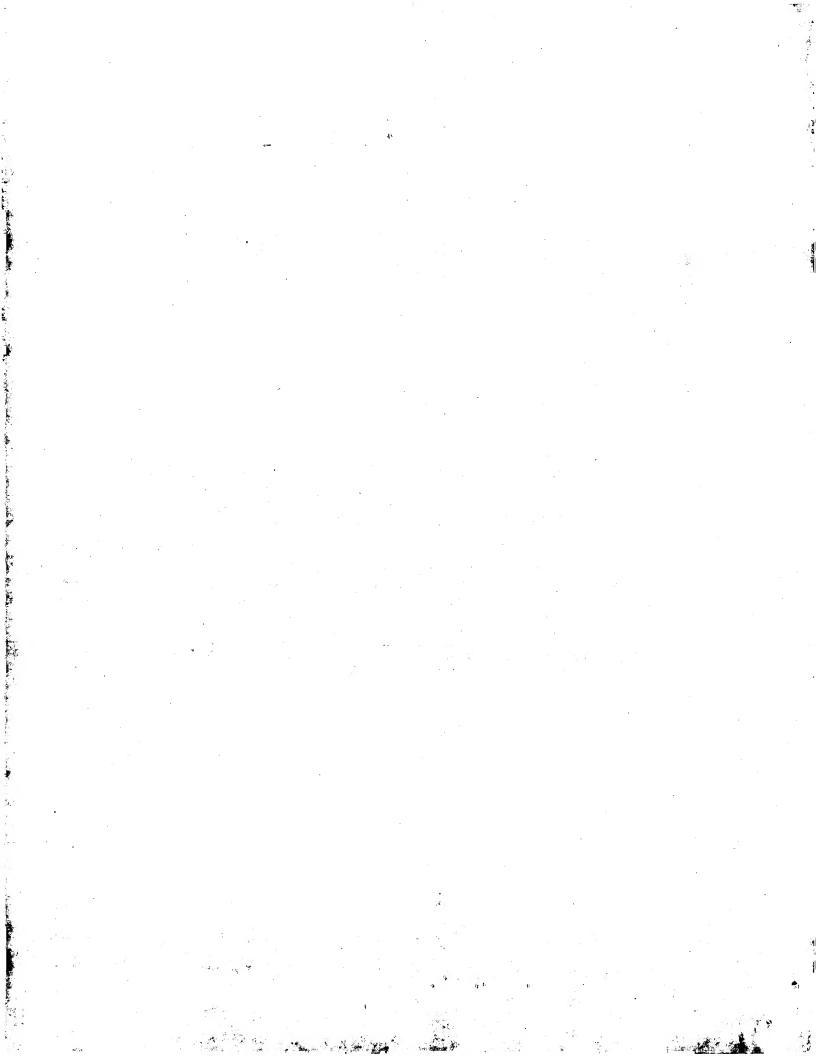
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02-FEB-2001
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Candida albicans agglutinin-like protein (ALS9) gene, partial cds.
AF229989
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I (bases I to 1404)
Hoyer, L.L., Hecht, J.E. and Mirus, K.A.
The ALS9 gene of Candida albicans
Unpublished
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Direct Submission
Submitted (31-JAN-2000) Veterinary Pathobiology, University Submitted (31-JAN-2000) Avenue, Urbana, IL 61802, USA Location/Qualifiers

1. .1404
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/note="first of a series of 108 bp repeat units'
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Pred. No. 1.6e-135;
0; Mismatches 366;
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/strain="1161"
/db_xref="taxon:5476"
/chromosome="6"
/map="60"
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286 c 253
                                                                  /gene="ALS9"
/codon_start=1
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73.8%;
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Best Local Similarity 73.8
Matches 1038; Conservative
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601 GIGGIGCCACAAIGIGAGAAIGGITACACAICIGGIAIAAIGGGAITITGIAGIAAC
                     GGTGACGTTGCTATTGATTGCTCAAATATTCATATTGGTATCACAAAAGGATTAAATGAT
                               721 TGGAATTATCCGGTTTCATCTGAATCATTTAGTTACACAAAAACTTGTACATCTAATGGA
                                                                       778 ATTACAGTIGAATTICAAAATGTICCIGCIGGGIATCGCCCTTTIGTIGAIGCATATATI
                                                                                                                                            841 TCTGCTACAGATGTTAACCAATATACTTTAGCATATACCAATGATTATACTTGTGCTGGC
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Human dentin sialo Cryptosporidium pa

dentin sialo

Candida

Probe Probe Нишап Kidney cancer rela Insert from cosmid Candida albicans-s

Candida albicans-s

Searched:

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Result

9

Sequence:

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Drosophila melanog Sequence encoding

Human immune syste

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C. albicans and C. stellatoides specific probes and primers - for specific detection of Candida infection
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Candida stellatoides; sputum; bronchial washings; blood; milk;
lymph fluid; skin; soft tissue; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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AAQ62592
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ABL25662
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ABL56203
ABL55643
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ABL33102
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                                           AAA61847
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16523.383 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                              **Carbaseq_101001:*

1. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

5. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

5. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

6. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

7. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

8. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

10. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

11. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

12. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

13. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

14. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

15. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

16. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

17. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

18. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

19. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

20. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

21. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

22. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

23. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

24. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

25. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

26. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

27. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

28. $SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 2185239 segs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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AAT32330
AAT32331
AAT32334
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AAT29063
                                                   OM nucleic - nucleic search; using sw model
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3786
1 atgcttcaacaatttacatt.
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Maximum DB seq length: 2000000000
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DNA sequence of pr Bacilius anthracis C. albicans Rbtl o Drosophila melanog Candida albicans-s Chicken leucocytoz AmEPV genome fragm AmEPV genome fragm Candida albicans-s

Human immune syste

Shatzman A;

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Livi GP,
  Hoyer LL,
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                                                                                                                                                                                                                                                            Gaps
                              Five synthetic sequences (AAT29063-67) are used as probes to detect the presence of Candida albicans and Candida stellatoides in biological fluids e.g. sputum, bronchial washings, blood, milk and lymph fluid or in tissue samples e.g. skin and soft tissues. The method of detection may also comprise using two of the probe sequences (AAT29065, AAT29066) as amplification primers and then detecting one of the probe sequences with the amplified product and detecting hybridisation.
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                                                                                                                                                         Score 359.2; DB 17; Length 424;
Pred. No. 4.6e-73;
0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer; detection; identification; Candida albicans;
a stellatoides; sputum; bronchial washings; blood; milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 424 BP; 126 A; 128 C; 67 G; 103 T; 0 other;
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          Figure 5B; 33pp; English
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                                                                                                                                                                     Best Local Similarity
Matches 376; Conserv
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          Claim 1;
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2164 CCAAACCATACTGTCACTACTACTGAATACTGGTCTCAATCATATGCTACAACCACCACT 2223
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                                       C. albicans and C. stellatoides specific probes and primers specific detection of Candida infection
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Pred. No. 2.4e-15;
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                                                                                                  Claim 1; Figure 5A; 33pp; English.
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Best Local Similarity 100.
Matches 108; Conservative
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WPI; 1996-300661/30
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1576 GTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAACCT
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                                                                                        Sequence 108 BP; 31 A; 30 C; 15 G; 32 T; 0 other;
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Pred. No. 2.4e-15;
0; Mismatches 0;
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100.0%; Pred. No. 2.4e-15;
live 0; Mismatches 0;
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100.0%;
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Matches 108; Conservative
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es 108; Conserv
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1624 CCAAACCCAACTGTCACCACCACTGAATATTGGTCCCAATCTTACGCAACCACAACTACT 1683
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Probe for Candida albicans and Candida stellatoides.
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tive 0; Mismatches 0;
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Candida stellatoides; sput
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2056 CCAAACCATACTGTCACTACTACTGAATACTGGTCTCAATCATATGCTACAACCACCACT 2115
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                                                                                                                                                                specific detection of Candida infection
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                 (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                               C. albicans and C. stellatoides specific probes and primers - for
specific detection of Candida infection
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               Probe; primer; detection; identification; Candida albicans; Candida stellatoides; sputum; bronchial washings; blood; milk; lymph fluid; skin; soft tissue; ss.
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                                                                                                                                                                                                                                                                                                                                             Hoyer LL, Livi GP, Shatzman A;
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      1 CCAAACCACACTGTCACTACTGAATACTGGTCACAATCATATGCCACCACTACCACT
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                                               Probe for Candida albicans and Candida stellatoides.
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99.1%; Pred. No. 5.5e-15;
tive 0; Mismatches 1.
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107; Conservative
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                                                                                                                                                      AAT32335 standard;
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biological fluids e.g. sputum, bronchial washings, blood, milk and lymph fluid or in tissue samples e.g. skin and soft tissues. The method of detection may also comprise using two of the probe sequences (AAT29066, AAT29066) as amplification primers and then contacting one of the probe sequences with the amplified product and
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Pred. No. 5.5e-15;
0; Mismatches 1; Indels 0;
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                                                                                                         Sequence 108 BP; 29 A; 29 C; 19 G; 31 T; 0 other;
                                                                                                                                     Score 108; DB 17;
Pred. No. 2.4e-15;
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                                                                                                                                  2.9%; Similarity 100.0%; Conservative 0;
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                                                                             detecting hybridisation.
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Matches 108; Conserv
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Detecting small integrin-binding ligand N-linked glycoproteins for detection of a tumor or protection against a complement mediated immune response, comprises detection where Factor H is not an inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of DNA encoding human dentin sialophosphoprotein (DSPP, see AAB1972), a member of the small integrin binding ligand, N-linked glycoproteins (SIBLINGS) family. The invention provides methods and compositions for exploiting the discovery that members of the SIBLINGS family bind to complement Factor H, conferring presistance to complement mediated lysis. A claimed method of conferring protection against a complement mediated immune response involves providing a reservoir or other suppert's body so that a SIBLINGS protein can be dispersed to interfere with complement mediated lysis and inflammation. This protects cells that are grafted onto foreign tissue or bone marrow cells introduced into a foreign host. The SIBLINGS protein can be BSP, OPN, DMPI or DSPP. A method of detecting a SIBLINGS protein in a sample from a subject suspected of having abnormal bone turnover, especially osteoporosis, is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1012 ACCACTGCTGTCACTTTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATGGAA 1071
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41.7%; Pred. No. 1.6e-11;
tive 0; Mismatches 823; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Five synthetic sequences (AAT29063-67) are used as probes to detect the presence of Candida albicans and Candida stellatoides in biological fluids e.g. sputum, bronchial washings, blood, milk and "lymph fluid or in tissue samples e.g. skin and soft tissues. The method of detection may also comprise using two of the probe sequences (AAT29065, AAT29066) as amplification primers and then centacting one of the probe sequences with the amplified product and detecting hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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integrin-binding ligand; diagnosis; antiinflammatory; therapy;
osteoporosis; chromosome 4; ds.
                                                                      Probe; primer; detection; identification; Candida albicans; Candida stellatoides; sputum; bronchial washings; blood; milk; lymph fluid; skin; soft tissue; ss.
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                                   Probe for Candida albicans and Candida stellatoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2332 GTTACTGCTCCTCCAGGTGGTACTGACACTGTGATTATC 2370
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2387. 7896
/*tag= a
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.
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pes 99; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     1432 GAATATTGGTCACAATCCTTTGCTACTACTACTGCTTACTGCTCCTCCAGGTGGTACT 1491
7110 ACTGCTGTCACTGCTATCGCTGTTGCTGCTGTCACTGCTGTCGCTGTTGCTATTGCTATC 7051
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                                            CATACTACCACAACTGTTACCAGTGAATGGACAGGAACAATCACTACCACCACAACTCGT
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Human; dentin sialophosphoprotein precursor; dentin sialophosphoprotein; DSPP; dentinogenesis imperfecta type II; deafness; auditory; chromosome 4q21; gene; ds.
2272 CCAAATCCAACAGTTACTACTACTGAATATTGGTCACAATCATTTGCCACAACCACCACA 2331
                 Human dentin sialophosphoprotein precursor (DSPP) gene SEQ ID NO:1.
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//note= "contains introns"
2387.2431
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/product= "phosphophoryn"

1252 ACCAATCCAACTGATTCAATTGACACAGTGGTGGTACAAGTTCCACTGCCAAATCCAACT

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7988..7993
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misc_feature
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Diagnosis of dentinogenesis imperfecta type III and its accompanying deafness using dentin sialophosphoprotein gene and encoded products

Example 3; Page 23-27; 38pp; Chinese

The present invention describes a method (M1) for the diagnosis of dentinogenesis imperfecta type II and/or its accompanying deafness comprising determining the dentin sialophosphoprotein (DSPP) gene, its transcript and/or protein of an individual for comparison of their sequences with the normal sequences and judging the individual to have higher risk of suffering from the disease then the normal population. Also described are: (1) treating dentinogenesis imperfecta type III and/or its accompanying deafness by administering a safe and effective dose of normal DSPP and/or DSP protein; and (3) a regent kit for detecting dentinogenesis imperfecta type III and/or its accompanying containing primers for specific amplification of DSPP gene or its transcript, or containing probes for binding to the mutation site. The DSPP gene and protein sequences have auditory activity. The method [71], dentin sialophosphoprotein (DSPP) gene and DSP protein are useful for for diagnosing and treating imperfects type II and/or its accompanying deafness. The DSPP gene is located to chromosome 4411. The present

Sequence 8201 BP; 2801 A; 1477 C; 1873 G; 2050 T; 0 other;

ö 1072 ATTITGCAACCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCC ACTGCTGTCACTGCTATCGCTGTTGCTGTTGCTGTCGCTGTCGCTGTTGCTATTGCTATT ACCACTGCTGTCACTTTACCATTCAATCCAAGTGTTGATAAAAACCAAAACGAA ATCGCTGCTGTCACTGCTGTTGCTGCTGTCACTACTATTACTGCTATCACTGCTGTCACT TATCTGACTAAGACTGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATAT CATACTACCACAACTGTTACCAGTGAATGGACAGGAACAATCACTACCACCACCACACTCGT ACTGCTGTCACTGCTGTTGCTGTCACCGCTATTGCTGCTGTCACTATTACTGCT Length 8201; Indels 1.5%; Score 94.2; DB 24; Similarity 41.7%; Pred. No. 1.6e-11; 88; Conservative 0; Mismatches 823; Best Local Sim Matches 588; Query Match 952 1012 7170 1132 7110 1192 7050 ò g ŏ g ò g à ò a

GTTACTGCTCCTCCAGGTGGTACTGACACTG 2362

2332

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2031 6211 1491 1551 6451 2091 2211 2271 6751 1672 ACCACAACTACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATTATCAGÁGAACCA GTCACTGCTATCACTGCTGTCACTGTCACTGCTATTGCTGCTATCACTACTATCACT GATACCGTTCTTATCAGAGAGCCACCAAACCATACTGTCACTACTACTGAATACTGGTCT 6150 ACTGCTGTCACTACTATCACTGCTGTTACTGCTATTGCTGTGTCGCTGTTATCACTGTT 2212 ACAACCACCACTGTTACTGCACCACCAGGTGGTACCGATACTGTTATCATTAGAGAGCCA 2272 CCAAATCCAACAGTTACTACTACTGAATATTGGTCACAATCATTTGCCACACAACCACACA 6990 GTCACTGCTATCACTGCTGTCACTGCTGCTGCTGTCACTGCTATTGCTGTTGTCACT 1312 GITAGIACTACTGAATAITGGTCTCAGICCTTTGCTACAACCACTACAGTTACTGCTCCT 1372 CCAGGTGGTACCGATACTGTGATTATCAGAGGCCACCAAACCATACTGTCACTACTACT 6870 GCTGCTATCACTGCTGTCACTATCACTGCTGCTGCTATCACTGCTGTGTCACTGCTATT GAATATIGGTCACAATCCTTIGCTACTACTACTGTTACTGCTCCTCCAGGTGGTACT GACTCAGTAATTATCAGAGAACCACCAAATCCAACTGTCACTACAACCGAGTATTGGTCT 1552 CAATCCTTTGCTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATT 1612 ATCAGAGAACCTCCAAACCCAACTGTCACCACCACTGAATATTGGTCCCAATCTTACGCA GCTGTCACTACTATTACTGCTGTCACTGCTATTGCTGCTGTCGCTATCACTGCTGTCACT 6570 GCTATCACTGCTATCACTGCTGTTGCTGCTATCACTGCTGTTGCTGCTATCACTGCTGTC CCAAACCACACTGTCACTACTGCTGCTGGTCACAATCATATGCCACCACTACCACT 6510 ACTGCTATTGCTGCTGTTGCTATCACTGCTGTTGCTGCTGTCACTACTATCACTGCT GTAACTGCACCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCACCAAACCACACT 6450 GTCACTGCTATCACTGCTGTCACTGCTGTTGCTGTCACTGCTACTGTCACT 1852 GTCACTACTACTGAGTATTGGTCTCAATCGTTTGCTACCAACAACTGTAACTGGTCCA GCTGTTGCTGCTGTCACTGCTGTCACTGCTGTCACTGCTATCGCTGTTGCTGCTGTTC 1912 CCAAGTGGCACTGATACTGTTATCATTAGGGAACCACCAAACCCAACTGTCACCACTACT ACTATCGCTGCTGTTACTATTACTGCTGTCACTACTATCACTGCTGTCACTATCACTGCT GAATACTGGTCTCAATCATATGCAACCACTACTACCATTACCGGTCCACCTGGTGAAACT General de la constanta de la c 2152 ATCAGAGAGCCACCAAACCATACTGTCACTACTGAATACTGGTCTCAATCATATGCT 1432 6810 1492 6390 6330 2032 6210 1972 qq q qq Dp δy qq g . <u>අ</u> Db pp δ q g ò g δλ à g ò 9 ò õ a ò a g ò 염 à ò ŏ δy ŏ Ω

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Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 other;
Iowa isolate of Cryptosporidium parvum.
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                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                            GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidiosis. Infection with Cryptosporidium is a common cause of diarrhoea in humans and causes life-threatening diarrhoea in humans compromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e.g., public symmuning pools). It is also a cause of disease in animals, resulting in financial losses in agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Cryptosporidium parvum Iowa isolate GP900"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900
                                                                                                                                                                                                                                                                    Cryptosporidium parvum Iowa isolate GP900 ORF
5910 GTCACTGCTATCACTGCTGTCACTG 5880
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93US-0071880.
92US-0891301.
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96US-0700651
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                                                                                                                               AAA61847 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Cryptosporidium parvum.
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                                                                                        RESULT 14
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986 CTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTACTTTACCATTCAATCCAA 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1286 TACAAGTTCCACTGCCAAATCCAACTGTTAGTACTACTGAATATTGGTCTCAGTCCTTTG 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                              1094 CCACGACAACTACAACCACAACCACAACTACCAAGAAACCAACAACAACAACAACAACAA 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1166 CTACTGTTATTGTTGATGTGCCATATCATACTACCACACTGTTACCAGTGAATGGACAG 1225
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Score 87; DB 21; Length 5511;
Pred. No. 6.4e-10;
0; Mismatches 330; Indels 0;
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hes 285; Conservative
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Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA
                                               Gut J;
                                                                                                                                   Disclosure; Page 99-101; 157pp; English
                                              Nelson RG,
         06-JUN-2000; 2000US-0588995
                           (REGC ) UNIV CALIFORNIA
                                               Barnes DA,
                                                                WPI; 2002-566447/60.
                                              Petersen C,
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The present invention relates to a method of detecting Cryptosporidium in biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for detecting and identifying individual Cryptosporidium isolates based on the genetic characteristics, and for diagnosis of prior or concurrent Cryptosporidium infection. The present sequence is a C. parvum coding sequence used in the exemplification of the invention.

Sequence 5511 BP; 1964 A; 1204 C; 944 G; 1399 T; 0 other;

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                                                                        CTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTATACCATTCAATCCAA 1045
                                                                                                1046 GTGTTGATAAAACCAAAACAATCGAAATTTTGCAACCTATTCCAACCACTACCATCACAA 1105
                                                                                                                                                                                    1034 CTACTACTACGACAACAACAACAACTACTACTACTACTACAACCACCACAACTACAA 1093
                                                                                                                                                                                                                         CTTCATATGTTGGTGTGTGACTTCCTATCTGACTAAGACTGCACCAATTGGTGAAACAG 1165
                                                                                                                                                                                                                                                            CCACGACAACTACAACCACAACCACAACTACCAAGAAACCAACAACAACAACAACAA 1153
                                                                                                                                                                                                                                                                                                  CTACTGTTATTGTTGATGTGCCATATCATACTACCACAACTGTTACCAGTGAATGGACAG 1225
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2.3%; Score 87; DB 24; Length 5511; 46.3%; Pred. No. 6.4e-10;
                               Conservative 0; Mismatches 330;
                 Best Local Similarity
Matches 285; Conserv
 Query Match
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Search completed: April 29, 2003, 17:29:43 Job time : 530 secs

103, App 43, Appl 41, Appl 49, Appl 45, Appl 59, Appl 59, Appl 51, Appl 51, Appl 61, Appl

Sequence Seq

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Sequence 1, Application US/08357962
Fatent No. 5668263
GENERAL INFORMATION.
APPLICANT: Hoyer, Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: SmathWilne Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDUNING TYPE: Diskette
           US-09-092-458-1

US-08-911-393-1

US-07-757-022B-13

US-07-757-022B-73

US-07-757-022B-73

US-07-757-022B-103

US-07-757-022B-103

US-07-757-022B-141

US-07-757-022B-41

US-07-757-022B-41

US-07-757-022B-45

US-07-757-022B-45

US-07-757-022B-59

US-07-757-022B-51

US-07-757-022B-51

US-07-757-022B-51

US-07-757-022B-51

US-07-757-022B-51

US-07-757-022B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ Version 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/357,962 FILING DATE: 16-DEC-1994 CLASSIFICATION TO TAKE A TO THE APPLICATION WHER: FILING DATE: APPLICATION WHER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P50278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1071 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Genomic
HYPOTHETICAL: NO
ANTI-SENSE: NO
linear
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-357-962-1
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Sequence 1, Appli
Sequence 5, Appli
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Sequence 2, Appli
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Sequence 3, Appli
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12900.869 Million cell updates/sec
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Sequence 3, A
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Sequence 32,
Sequence 34,
Sequence 34,
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                                                                                       April 29, 2003, 16:36:22; Search time 90 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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S-08-145-705A-33
S-08-145-705A-36
S-09-165-239A-3
S-08-145-705A-35
S-08-145-705A-35
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US-08-978-106-5
US-08-928-3618-2
US-08-928-3618-1
US-08-928-3618-1
US-08-928-3618-4
US-08-928-3618-4
US-08-928-3618-3
US-08-357-962-2
US-08-377-962-2
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Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
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Maximum DB seq length: 200000000
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linear
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APPLICANT: HOYER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-878-106-1
                                                                                                                                                                                                                          USA
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  DB 1; Length 1071;
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                         Indels
 Score 1069.4; DB 1
Pred. No. 5.8e-252;
0; Mismatches 1;
28.2%;
ilarity 99.9%;
Conservative (
             Similarity
                      Matches 1070;
   Query Match
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1021 ACAACCACCACAGTTACTGCTCCTCCAGGTGGTACTGACACTGTGATTATC 1071
                                                                                                                                                                                                     APPLICANT: Livi, George
PPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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0; Mismatches 1;
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Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,106
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,962
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                     Sequence 1, Application US/08878106
Patent No. 5817466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31,171
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REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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LENGTH: 1071 base pairs
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline |
STREET: 709 Swedeland |
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Matches 1070; Conservative
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                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia
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                                                                                                                                                                                        Hoyer, Lois
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Query Match
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Matches
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                                                                                     CAATCTTACGCAACCACAACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATT 1719
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                                                                                                                                                                                                                     CCAAACCACACTGTCACTACTACTGAGTATTGGTCTCAATCGTTTGCTACTACCACAAACT 1899
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                                                      2140 GATACCGTTCTTATCAGAGGCCACCAAACCATACTGTCACTACTGCTGAATACTGGTCT
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            241 GAGTATTGGTCTCAATCCTTTGCTACTACTACAGTTACTGCTCCTCCTCCAGGTGGTACT
                                          GACTCAGTAATTATCAGAGAACCTCCAAACCCAACTGTCACCACCACTGAATATTGGTCC
                                                                                                           CAATCTTACGCAACCACAACTACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATT
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                                                                                                                                                                          ACCACTACCACTGTAACTGCACCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCA
                                                                                                                                                                                                                                CCTGGTGAAACTGATACCGTTCTTATCAGAGGCCACCAAACCATACTGTCACTACTACT
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APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TILE OF INVENTION: CONSERVED YEAST NUCLEIC
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
Shatthkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08357962
Patent No. 5668263
GENERAL INFORMATION:
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STATE: PA
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                                                                    SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,962
FILING DATE: 16-DEC-1994
CLASSIFTAMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08878106
Patent No. 5817466
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TELEFAX: 610-270-509
                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 425 base pairs
TYPE: nucleic acid
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ZIP: 19406-0939
COMPUTER READABLE FORM:
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es 376; Conserv
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 CTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTACTTTACCATTCAATCCAA 1045
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6.3%; Pred. No. 9e-12;
ve 0; Mismatches 330; Indels
                         381 CTCCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGT
  2339 CTCCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                   PETERS, VERNY, JONES &
                                                                                                                                                                                                                                                                                                                                                                      385 Sherman Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                            ; Sequence 2, Application US/08928361B; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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REGISTRATION NUMBER: 30,518
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TELEPHONE: 650-324-1677
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Matches 285; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                        TITLE OF INVENTION: PY
TITLE OF INVENTION: FY
TITLE OF INVENTION: FY
TITLE OF INVENTION: FO
                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Petersen,
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                                                                                                                                                                                                                                                                                                                                                                      STREET:
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Hoyer, Lois
Livi, George
Shatran, Allan
VENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
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Pred. No. 5.5e-76;
0; Mismatches 28;
                                                       TITLE OF INVENTION: CONSERVED YEAST NUCLEIC AC NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STREE: PA COUNTRY: USA ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P50278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/357,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/35
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.2
Best Local Similarity 92.8
Matches 376; Conservative
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610-270-5090
                                                                                                                                                                                                                                                                                    COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: FastSEC
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; CRIGINAL SOURCE:
US-08-878-106-5
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                                      APPLICANT:
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GLYCOPROTEINS, DNAS AND RNAS
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APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CORRENT FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-04-03
SUPPRAIRE FILING DATE: 1995-04-03
SUPPRAIRE: PATEUTION NOS: 15
SOFTWARE: PATEUTIN VET. 2.0
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                                                                                       986 CTACAACTAGAACAGTTACAGACAGTACCACTGCTGTCACTATTACCATTCAATCCAA 1045
                                                                                                              1046 GTGTTGATAAAACCAAAACAATCGAAATTTTGCAACCTATTCCAACCACTACCATCACAA 1105
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Score 87; DB 3; Length 733
Pred. No. 1e-11;
0; Mismatches 330; Indels
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; ORGANISM: Cryptosporidium parvum
US-08-700-651-1
                      46.38;
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                    Best Local Similarity 46.3
Matches 285; Conservative
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Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
                                           1286 TACAAGTTCCACTGCCAAATCCAACTGTTAGTACTACTGAATATTGGTCTCAGTCCTTTG 1345
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1214 CTACTACTACTACTACTACCACAACCACAACCACAACCACAACTACCAAGAAACCAA 1273
                                                                                    1274 CAACAACAACAACAACAACAACAACTACTACTACTACCACGACAACAACAACAGGGG 1333
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
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REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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APPLICATION NUMBER: US 60/026,062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13-SEP-1996 ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION: THE
TITLE OF INVENTION: SPE
TITLE OF INVENTION: SPE
COMBER OF EXQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VE
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US-08-928-361B-1
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                                                             189 AAGGTTATAGCATTGATTCATCCACCGGGTTTAGAGTTGATTCTATCACTGGTCTCCCAA 248
                                                                                                                                                         CTGATCCAT--ACTCTAATTGTCCATTCAACCTGTCACTGGAAATTTAGTCAGTAGGTC 306
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 Length 5163;
                               Indels
; DB 3;
1.4e-11;
                             0; Mismatches
Score 86.2;
Pred. No. 1.
. 2.38;
                             Conservative
              Similarity
                            Matches 496;
Query Match
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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                     306 CACTGGTAAAACTATTCCAAACACTTATGCAGGTGTTTATCGTTCTAATGAGACTAAGAC
ATCATATGCAACCACTACCATTACCGCTCCACCTGGTGAAACTGATACCGTTCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES &
ADDRESSEE: 385 Sherman Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                        Sequence 4, Application US/08928361B Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 496; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: Peters
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STATE:
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND FITLE OF INVENTION: FOR PROPHILAXIS AND TREATMENT OF CRYPTOSPORTION OF TITLE OF INVENTION: FOR PROPHILAXIS AND TREATMENT OF CRYPTOSPORTION OF TITLE OF INVENTION: FOR PROPHILAXIS AND TREATMENT OF CRYPTOSPORTION OF TITLE OF INVENTION OF TITLE OF INVENTION OF TITLE OF TITLE OF THE PETERSENCE: 480-194-104
CURRENT APPLICATION NUMBER: US/08/700,651B
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER REILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTGTTATCATTAGGGAACCACAAACCCAACTGTCACCACTACTGAATACTGGTCTCA 1985
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                            TTCAATTGACACAGTGGTGGTACAAGTTCCACTGCCAAATCCAACTGTTAGTACTACTGA
                                                                                 ATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGTACCGA
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                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                       Pred. No.
                                                  TYPE: DNA ORGANISM: Cryptosporidium parvum
                                                                                                                                                         2.3%;
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                                                                                                                                                                                    Similarity
                         5318
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SEQ ID NO 2
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1146 TGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCACAAC 1205
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APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SmithKline Beecham Corporation
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Patent No. 5668263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hoyer, Lois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-357-962-2
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TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATHENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
1926 TACTGTTATCATTAGGGAACCACCAAACCCAACTGTCACCACTACTGAATACTGGTCTCA 1985
                                                                                  CTTTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATCGAAATTTTGCAACCTATTC 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA--ACCACTACCATCACAACTTCATATGTTGGTGTGTGACTACTTCCTATCTGACTAAGAC 1145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 1.4e-11;
); Mismatches 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: PETERS, VERNY, JONES & BIKSA
385 Sherman Avenue, Suite 6
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12-SEP-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
                                                                                                                                                                                                                                                                                    US/08928361B
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REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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Similarity 46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
" NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
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LENGTH: 5318 base pairs
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Best Local Similarity 46.0
Matches 496; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 12-SEP
                                                                                                                                                                                                                                                                                  Sequence 3, Application
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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STATE:
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1300 CCAAATCCAACTGTTAGTACTACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACA 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RTDACYGSWCCWCCWRGHACYGAYWCHGTDMTYATYAGRGARCW 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Springer, Wolfgang; Plempel, Manfred; APPLICANT: L bberding, Antonius TITLE OF INVENTION: SPECIFIC GENE PROBES AND TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC TITLE OF INVENTION: INVESTIGATION OF CANDIDA TITLE OF INVENTION: ALBICANS
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score 85.2; DB 1;
60.2%; Pred. No. 5.4e-12;
tive 41; Mismatches 2;
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APPLICATION NUMBER: German P 42 36 708.5
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SPRONG HORN KRAMER & WOODS STREET: 660 White Plains Road CITY: Tarrytown
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CURRENT APPLICATION LATA:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
                      APPLICATION NUMBER: US/08/878,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08145705A Patent No. 5489513 GENERAL INFORMATION:
                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,962
FILLING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TELEFAX: 610-270-5090
                                                                                                                                                                                                31,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                         NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 60.2%
Matches 65; Conservative
CURRENT APPLICATION DATA
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ORIGINAL SOURCE:
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US-08-145-705A-32/c
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STATE:
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APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1360 GTTACTGCTCCTCCAGGTGGTACCGATACTGTGATTATCAGAGAGCCA 1407
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2.3%; Score 85.2; DB 1;
Best Local Similarity 60.2%; Pred. No. 5.4e-12;
Matches 65; Conservative 41; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/357,962
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P50278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08878106
Patent No. 5817466
GENERAL INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                          COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PILING DATE:
ATRODAMEN ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                    King of Prussia
                                                                                                                                                                                                                                                           FILING DATE: 16
CLASSIFICATION:
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ORIGINAL SOURCE:
US-08-357-962-2
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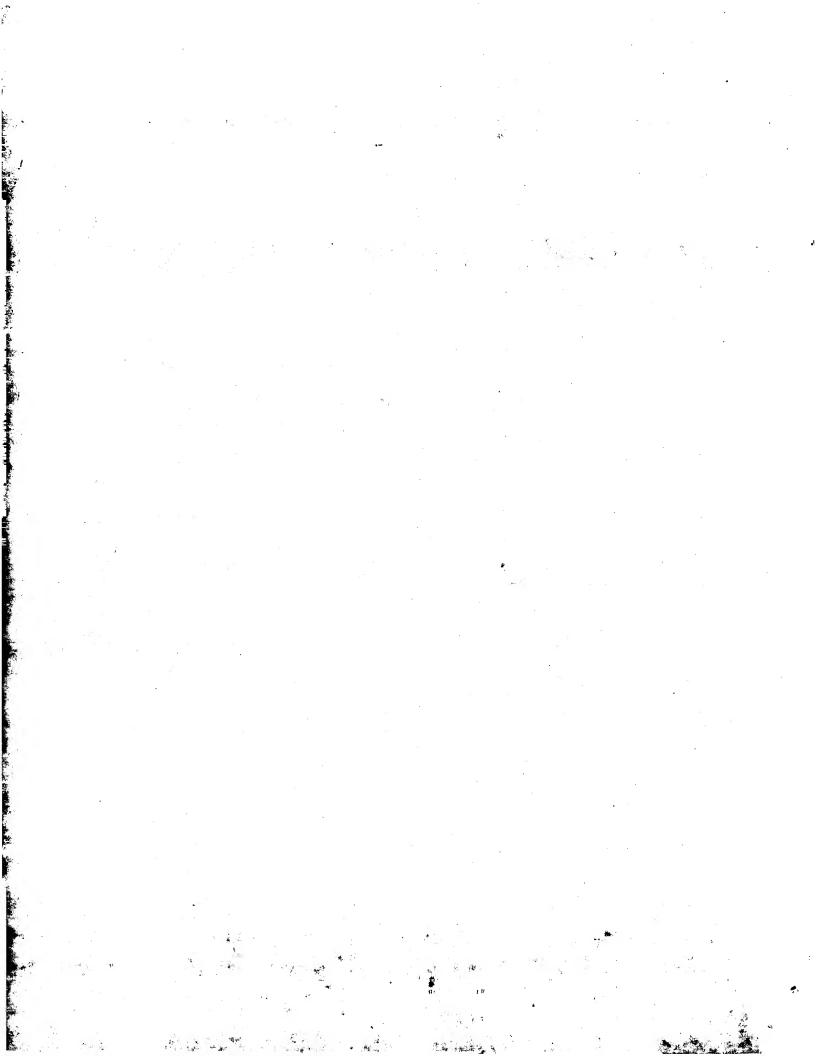
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2.2%; Score 82.4; DB 1; Length 100; 89.0%; Pred. No. 2.5e-11; tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage COMPUTER: NEC PowerMate 1 Plus OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                1030 TTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATCG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: L bberding, Antonius
TITLE OF INVENTION: SPECIFIC GENE PROBES AND
TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
TITLE OF INVENTION: INVESTIGATION OF CANDIDA
TITLE OF INVENTION: ALBICANS
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 TTACCATTCAATTCCGATGTTGACAAAACTAAAACAATTG 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: German P 42 36 708.5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SPRUNG HORN KRAMER & WOODS
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08145705A Patent No. 5489513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,141
                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                             ; ORGANISM: Candida albicans
US-08-145-705A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (914) 332-1700 TELEFAX: (914) 332-1844
  LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.0°
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 100 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  SEQUENCE CHARACTERISTIC;
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ADDRESSEE: SPRUNG HO
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MOLECULE TYPE: DN
                                                                                                                         HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-145-705A-33/c
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                                                                                                                                                                                                                                                                                                                                                                                                                            2.2%; Score 82.4; DB 1; Length 100; 89.0%; Pred. No. 2.5e-11; tive 0; Mismatches 11; Indels
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ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage COMPUTER: NEC POWERMATE 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
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Patent No. 5489513
GENERAL INFORMATION:
APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: L bberding, Antonius
TITLE OF INVENTION: SPECIFIC GENE PROBES AND
TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC
TITLE OF INVENTION: INVESTIGATION OF CANDIDA
TITLE OF INVENTION: ALBICANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AATCACTACTACTACAACACAAACTAATCCAACAGGTTCA 1
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               REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bayer 8885-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SPRUNG HORN KRAMER & WOODS STREET: 660 White Plains Road CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,141
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TELECOMMUNICATION INFORMATION
TELEPHONE: (914) 332-1700
                                                                                                                                           INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 100 base pairs TYPE: nucleic acid stranbedness: single
                                                                                                                                                                                                                                                                                                                                                                 Candida albicans
                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Matches 89; Conservative
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Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO CRIGINAL SOURCE: CARCANISM: CANCUS-145-705A-32
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US-08-145-705A-34/C
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Sequence 1748, Ap Sequence 19481, A Sequence 6291, Ap Sequence 19383, A Sequence 13, Appl Sequence 13, Appl Sequence 83, Appl

13, Appl 83, Appl 73, Appl 57, Appl 103, Appl 43, Appl

Sequence 73, Appl Sequence 103, Appl Sequence 103, Appl Sequence 41, Appl Sequence 141, Appl Sequence 45, Appl Sequence 59, Appl Sequence 75, Appl Sequence 71, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl

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Sequence:

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1309 ACTGTTAGTACTACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTTACTGCT 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chuenkova, Marina
APPLICANT: Chuenkova, Marina
APPLICANT: Pereira, Miercio A.
TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and
FITLE OF INVENTION: Methods of Use Therefor
FILE REFERENCE: 1322.1028-001
CURRENT APPLICATION NUMBER: US/09/745,008
CURRENT FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78.4; DB 10; Length
Pred. No. 4.2e-07;
0; Mismatches 606; Indels
             US-09-880-107-1748
US-09-864-761-19481
US-09-815-242-4580
US-09-815-242-8291
US-09-864-761-19383
US-10-124-557-13
US-10-124-557-33
US-10-124-557-103
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US-10-044-090-303
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US-10-124-557-45
US-10-124-557-59
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US-10-124-557-39
US-10-124-557-51
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US-10-124-557-41
US-10-124-557-14:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 5403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/09745008 Patent No. US20020137667A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.18;
   ; TYPE: DNA
; ORGANISM: Trypanosoma cruzi
US-09-745-008-33
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442; Conservative
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Query Match
Best Local Si
Matches 442
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Sequence 285. Appl
Sequence 340, Appl
Sequence 343, Appl
Sequence 345, Appl
Sequence 107, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 1058, Appl
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Seguence 1, Appli
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15906.005 Million cell updates/sec
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is derived by analysis of the total score distribution.
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3786
1 atgcttcaacaatttacatt......tgtccttgttcatttagtga 3786
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// cgnz_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
// cgnz_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
// cgnz_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
// cgnz_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
// cgnz_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                                                                                                          April 29, 2003, 19:18:29; Search time 259 Seconds
                GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-216-393-340

US-09-216-393-343

US-09-216-393-345-3

US-09-216-393-345-3

US-09-216-393-345-3

US-10-073-256-54-3

US-10-073-256-54-3

US-10-025-380-1058-3

US-09-842-552-79-3

US-09-842-552-79-3

US-10-025-380-1058-3

US-09-922-217-1058-3
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US-09-137-531-7
US-09-137-531-8
US-09-955-909-1
US-09-822-846-491
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74.4; DB 10;
Pred. No. 4.9e-05;
0; Mismatches 801;
                                                                                                                                                                                                                                                 CLASSIFCATION:
ATTORNEY, AGENT INFORMATION:
NAME: MCMMSters, David D.
NEGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECHOMONICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELEFAX: (206) 682-490
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 684973 base pairs
                                                                                                                                                                                         UMBER: US/09/263,959
05-MAR-1999
                                                                                                                 PC-DOS/MS-DOS
                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS.
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Matches 626; Conservative
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TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES 1279
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
1549 TCTCAATCCTTTGCTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA 1608
                                                                                                                                                                                                                                                                                        ACTGTGGGCACTGCTGTCAACGGGAGTTGAGGGCGTACTGTGGGGCACTGCTGTCAGCGGG 3370
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                                                                                                              ATTATCAGAGAACCTCCAAACCCAACTGTCACCACCACTGAATATTGGTCCCAATCTTAC 1668
                                                                                                                                                                                                                               GCAACCACAACTACTGTGACTGCTCCTCCAGGAGGCACTGACTCAGTAATTATCAGAGAA 1728
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6300 Columbia Center, 701
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STATE: Washington
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                                                                                              Score 62.2; DB 10;
Pred. No. 0.00093;
0; Mismatches 548;
                                                                                                Query Match 1.6%;
Best Local Similarity 42.3%;
Matches 402; Conservative
                                     ; ORGANISM: Bacillus anthracis
US-09-842-552-22
LENGTH: 2014
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Sequence 22, Application US/09842552

Batent No. US2002055528A1

GENERAL INFORMATION:

RELATE OF INVENTION:

RELATED BACTERIA

TITLE OF INVENTION:

RELATED BACTERIA

FILE REPERENCE: 5-89,687

CURRENT APPLICATION NUMBER: US/09/842,552

CURRENT FILIG DATE: 2001-04-23

PRIOR PILICATION NUMBER: US 60/199,911

PRIOR FILING DATE: 2000-04-26

SOFTWARE: PALENTIN VERSION 3.0

SEQ ID NO 22
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                                     CTACAAATACTGCTGATGCTAACACTAGTAATACTGTTCCTAATACCACTATGCCTTCTC 13284
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  CAAACCATACTGTCACTACTACTGAATATTGGTCACAATCCTTTGCTACTACTACTACTG 1468
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DEFLICANT: Milhausen, Michael James

TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: TX-1-C2

CURRENT APPLICATION NUMBER: US/09/216,393

CURRENT FILING DATE: 1998-12-18

EARLIER APPLICATION NUMBER: 08/994,825

EARLIER FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 364

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 340
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                                                1025 CTACTTTACCATTCAATCCAAGTGTTGATAAAACCAAAACAATCGAAATTTTGCAACCTA 1084
                                                                                                                                                                                                                                                                                                                                             1145 CTGCACCAATTGGTGAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCACAA 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 CTACTAATACTATCATTACCACTACTATTACCATTACCACGACTATCATTACTACTA 187
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                                                                                              68 CTATTGTCACTACTATTACCACTACCATTAGTACTACCACCACCATTATCATCATCACTACCATCA 127
  Gaps
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0; Mismatches 161; Indels
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Pred. No. 0.028;
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Best Local Similarity 45.5%;
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ORGANISM: Toxoplasma gondii
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Conservative
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US-09-216-393-340
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Matches 152;
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                                                                                                                                                                                                                  PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEI
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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EXPRESSED IN BONE MARROW, SIGNAL = 1.5
EXPRESSED IN HELA, SIGNAL = 1.2
EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
EXPRESSED IN LONG, SIGNAL = 1.2
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IN HBL100, SIGNAL = 1.
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LENGTH: 436
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Pred. No. 0.013;
                                                                                                                                                                                                                                                                                       FILE REFERENCE: Aeomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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ING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00670
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G DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                  CATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/234,687
                                                                  Application US/09864761
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PLICATION NUMBER: GB 24263.6
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NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE:
PRIOR APPLICATION NO
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US-09-864-761-2885
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APPLICANT: Milhausen, Michael James
APPLICANT: Milhausen, Michael James
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT APPLICATION NUMBER: 08/994,825
EARLIER APPLICATION NUMBER: 08/994,825
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PAGE IN VOY: 2.0
SEQ ID NO 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 345, Application US/09216393
Petent No. US20010014447A1
GENERAL INFORMATION:
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT PILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3077 CAAACTCCATCACTGAAGATATCACCACATCTCAACCTACAGGTGATAATGGAGACAATA 3136
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Pred. No. 0.036;
                                          Sequence 343, Application US/09216393 Patent No. US20010014447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%;
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Toxoplasma gondii
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US-09-216-393-343
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1052 CAACGACTA 1060
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                       US-09-216-393-343
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TITLE OF INVENTION: TOXOLESA COMES
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 342
LENGTH: 867
                                        CTCCATCACCTGCTTTCTTCTGGTACTGATGTAACTACTGAACCAACTGATACTAGAG 3376
                                                                                                                     3077 CAAACTCCATCACTGAAGATATCACCAÇATCTCAACCTACAGGTGATAATGGAGACAATA 3136
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635 CTACACCAACAACAACAACAACAACAACAACGACAACTACAACGACATCTACGACAACCA 694
                                                                               695 CTACGACTACCACAACTACTACTACAACTACAACAACGACGACCACGGAACCAACAA 754
                                                                                                                                            CTGCGTTCATTAGGCCAAGGAGGTCAAAGAGGGGAAAAAGGACTACAACTACAACCAGTT 454
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Pred. No. 0.028;
0; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                               Sequence 342, Application US/09216393
Patent No. US2001001447A1
PERERAL INFORMATION:
APPLICANT: Milhausén, Michael James
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Best Local Similarity 45.5%;
Matches 195; Conservative
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; ORGANISM: Toxoplasma gondii
US-09-216-393-342
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815 CAACGACTA 823
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US-09-216-393-342
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SOFTWARE: PatentIn version 3.0
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Matches 335; Conserv
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                                                                                    US-09-801-368-107
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                   SEQ ID NO 107
LENGTH: 410
                                                                                                                       Query Match
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                                                                                                                                                   Score 54.6; DB 10;
Pred. No. 0.036;
0; Mismatches 234;
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TITLE OF INVENTION: Methods for Improving
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CURRENT PAPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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Milne, Todd
No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
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Patent No. US20020128250A1
GENERAL INFORMATION:
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 345
LENGTH: 1397
                                                                                                                                                    Query Match 1.4%;
Best Local Similarity 45.5%;
Matches 195; Conservative
                                                                                   TYPE: DNA ORGANISM: TOXOPlasma gondii
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hottzman, Doug
APPLICANT: Madden, Kevin
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Sherman, Amir
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Sequence 54, Application US/10073256
Patent No. US20020120408A1
GENERAL INCORMATION:
APPLICANT: Kreiswirth, Barry N
APPLICANT: Nadich, Steven M
TITLE OF INVENTION: System and Method for Tracking and Controlling Infections
FILE REFERENCE: 19124.0002
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                                                                                                                                Length 4104;
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                                                                                                                      1.4%; Score 52.8; DB 10;
ilarity .43.7%; Pred. No. 0.17;
Conservative 0; Mismatches 422;
TYPE: DNA ORGANISM: Saccharomyces cerevisiae
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APPLICANT
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                                                                                                                                                                                                                                                                                             1303 AATCCAACTGTTAGTACTACTGAATATTGGTCTCAGTCCTTTGCTACAACCACTACAGTT 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      770 TCTGAGTCGCTGTCTGAATCTGAATCGCTGTCTGAGTCCGAATCGCTATCTGAATCTGAG 711
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Pred. No. 0.11;
0; Mismatches 468;
CURRENT APPLICATION NUMBER: US/10/073,256
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
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                                                                                                      ; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-073-256-54
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Matches 333; Conservation
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RESULT 11 US-09-842-552-79/C

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APPLICATE: The Regents of The University of California
TITLE OF INVENTION: MULTILOCUS REPETITIVE DNA SEQUENCES FOR GENOTYPING BACILLUS A:
TITLE OF INVENTION: RELATED BACTERIA
FILE REPERBENCE: 5-89,687
CURRENT APPLICATION NUMBER: US/09/842,552
CURRENT FILING DATE: 2001-04-23
PRIOR PAPLICATION NUMBER: US 60/199,911
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
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Pred. No. 0.17;
0; Mismatches 155; Indels
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Sequence 79, Application US/09842552
Patent No. US20020055628A1
GENERAL INFORMATION:
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Stolk, John A.
Wang, Tongtong
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Skeiky, Yasir A. W.
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
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Vedvick Thomas S.
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Best Local Similarity 48.3%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Bacillus anthracis
US-09-842-552-79
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
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Smith, Carole L.
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SOFTWARE: FastSEQ for Winds
SEQ ID NO 1058
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RESULT 14
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                                                                                               Gaps
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                                                                    Length 15720;
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                                                                                            Indels
                                                                 Score 50.8; DB 9;
Pred. No. 0.98;
0; Mismatches 342;
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Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
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Smith, Carole Lynn
                                                                   1.3%;
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
                                                                   Query Match
Best Local Similarity 43.8
Matches 269; Conservative
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Wang, Aijun
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            ; TYPE: DNA
; ORGANISM: HOMO
US-10-025-380-1058
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LENGTH: 15720
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TITLE OF II
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Sequence 1058, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: Infanosis of Colon Cancer And Methods FOR THEIR USE
FILE REFERENCE: 210121.471012.
CURRENT APPLICATION NUMBER: US/09/833,263
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Pred. No. 0.98;
0; Mismatches 342;
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1058
LENGTH: 15720
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Best Local Similarity 43.8%;
Matches 269; Conservative
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CRGANISM: Homo sapiens
US-09-922-217-1058
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Publication No. US20030073610A1
GENERAL INFORMATION:
APPLICANT: LINDQUIST, SUSAN
APPLICANT: LINDQUIST, SUSAN
APPLICANT: OUTERO, TIAGO F.
TITLE OF INVENTION: YEAST SCREENS FOR THE TREATMENT OF HUMAN DISEASE
FILE REFERENCE: ARCD:367US
CURRENT APPLICATION NUMBER: US/10/077,584
CURRENT FILING DATE: 2002-02-15
PRIOR FILING DATE: 2001-02-15
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Pred. No. 0.98;
0; Mismatches 342;
             NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1058
LENGTH: 15720
2001-04-10
                                                                                                                                            1.3%;
Similarity 43.8%;
59; Conservative
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                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-263-1058
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CURRENT FILING DATE:
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Pred. No. 0.26;
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Job time : 569 secs
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1236
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                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Matches 143; Conserva
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; LOCATION: (1)..(513)
US-10-077-584-3
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T7 end of Tetraodon SP\_1005\_A Fugu rubr

Fugu rubr F.rubripe fv51b11.y CH230-81P

Tetraodon

AL40548 7 AL171639 7 AZ185454 5 AL444958 1 AL444958 1 AL444858 1 AL018519 1 BM181884 4 BM355163 6 AZ166409 5

09 SP\_0088\_A 86 Fugu rubr CpG0015B Cp 85 Tetraodon

SP\_0076\_B ht47h12.9 Av973760

Total number

Database

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Searched:

Sequence:

SP\_1039\_B fzmb013f0 1M0502E21

Ciona int EST572587

SP\_0100\_A BJ388152

AZ205202 BJ388152

Fugu rubr

F.rubripe fk95c07.y T7 end of Fugu rubr 2M0246M24 rubripes EST572669

AL44251 F AL004959 F BE556771 AL409242 T AL130699 F AZ972907 Z 289848 F.I

Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis

Dujon, B.

TITLE

Result Š.

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SP\_0100\_A F.rubripe

AV973760 A AZ183942 BAB81398 A AZ011359 A AC011359 B AZ199472 AZ140388 A AZ240388 A AZ240388 A BM170064 B

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Run on:

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Candida tropicalis.

Candida tropicalis.

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Candida tropicalis.

Sucarycota: Fungi; Ascomycota; Saccharomycotlans; Saccharomyceteles; Saccharomycetales; Candida.

L (bases 1 to 959)

S Souclard, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

L FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                           AL444386 Fugu rubr
B67199 CpG0015B Cp
AL225985 Terraodon
290754 F. rubripes
BM605179 170006870
AZ434703 1M0221C24
AZ164800 SP_0076_B
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BH881398
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A2972907
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                                                                                  April 29, 2003, 17:19:18 ; Search time 3337 Seconds (without alignments) 18374.622 Million cell updates/sec
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Compugen Ltd.
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           GenCore version Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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                                                                                             Libert Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: Sequencepe.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ratuyeri, Riuyveromyces thermotoclarans, Kluyveromyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces hansenii Aluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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/strain="CBS 94"
/db.xref="taxon:5482"
/clone="Bb0AA010H12"
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FEBS Lett. 487 (1), 91-94 (2000)
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/note="end : T3"
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 BVRY cedex, FRANCE. (E-mail: seqref@qenoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces ervazzii, Zygosaccharomyces rouxii, Saccharomyces Kluyverl, Kluyveromyces thermotolerans, Kluyveromyces
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
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T7 end of clone BD0AA009G07 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
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[bases] Lo 83;
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lhorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.,
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FEBS Lett. 487 (1), 3-12 (2000)
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lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers

1. 893
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                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                   /organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BDOAA009G07"
/clone_lib="BDOAA"
/note="end:T7"
                                                                                                                                                                                                                                                                                                                         9.3%; Score 353; DB 17;
llarity 66.4%; Pred. No. 3.3e-80;
Conservative 2; Mismatches 274;
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqreféqenoscope.cns.fr - Web :
Fris GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces tartis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this sequence and for the sequence of the other extremity of this insert.
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T7 end of clone BD0AA004B02 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
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l (bases 1 to 1050)

Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano. Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1050)
Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F.
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FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                  2302
   2242
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                                                               196 CCACCGAATATGGATCTGTTTCTGAACCAACCACCATCACATATACCAACCCACCAGGTG
                                                                                                                                  2243 GTACCGATACTGTTATCATTAGAGACCCACCAAATCCAACAGTTACTACTACTGAATATT
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/clone_lib="BD0AA"
/note="end : T7"
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Candida tropicalis
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75 GATTATGCAACTAGGGTTACTGAGACACATGGTCCAGACCAAACTGATGTTGTTGT
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complement(<7. .>921)
/note="s.lmilar to 013368 [ Agglutinin-like protein ALA]
precursor ] [ Candida albicans]"
/evidence=not_experimental
a 185 c 226 g 336 t 2 others
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                                                                                                                                                                                                                                    AATCCAAGTGTTGATAAAACCAAAACGAAATTTTGCAACCTATTCCAACCACTACC 1098
                                                                                                                                                                                                                                                                                              ATCACAACTTCATATGTTGGTGTGACTACTTCCTATCTGACTAAGACTGCACCAATTGGT 1158
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                                                                                                                             2.3e-59;
                                                                                                           7.2%; Score 272.8; 56.1%; Pred. No. 2.3
                                                                                                                                            Conservative
                                                                                                                           Similarity
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   misc_feature
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                                                                                                             Query Match
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L. Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web:
rhis GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzil, Zygoasccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
     17 end of clone BDOAA009H06 of library BDOAA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
                                                                                                                                                                                                                                                                                    1 (bases 1 to 1047)
Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregolā, S.,
Ge-Montigny, J., Dion, B., Durens, P., Lepingle, M., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1047)
Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<2. .>484)
/note="similar to 074660 { Agglutinin-like protein 4
precursor, ALS4 ] [ Candida albicans]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 2.7e-31;
0; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Candida tropicalis"
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178 c 171 g 322
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/clone_lib="BD0AA"
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Best Local Similarity 60.55
Matches 291; Conservative
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Direct Submission
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exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyverii, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
    uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 CCAGGGGATACATTCACATTGAATATGCCATGTGTGTTTAAATATACTACTTCACAAACA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTTTGATAGTTTTAATTCATTAACTTGGTCCAATGCTGCTAATTATGCTTTCAAAGGG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AGAATTCACAACTTTTTCTACATTAACATGTACTGTGAACGACGCTTTGAAATCATCCAT 365
                                                                                                                                                                                                                                                                                                                      /clone__lib="BD0AA"
/note="end : T7"
6552. .>988
/note="similar to P46590 [ Agglutinin-like protein 1 precursor, ALS1 ] [ Candida albicans]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 TCTGTTGATTTAACTGCCGATGGTGTTAAATATGCTACTTGTCAATTTTAT-TCTGGTGA
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4; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
  bayanus var.
                                                                                                                                                                                                                                      /organism="Candida tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%; Score 144.4;
62.6%; Pred. No. 4.5
                                                                                                                                                                                                                                                         /strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0AA010H12"
yeast species: Saccharomyces
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AL299119.1 GI:8038260
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Matches 234; Conservative
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
sequef@genoscope.cns.fr - Web:
This GSS is part of a random genomic sequencing program of thirteen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO7DAY 1011 bp DNA linear GSS 08-JUL-2001 T7 end of clone BD0AA010H12 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence. AL40240.
AL40240. GI:12223651
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[ bases 1 to 1011)

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano. Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F.
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                                                                                                                                                                                                                                                                                                      243 CAAATCAAAACACTGTTGATTTGATTGCTGATGGCACTACTAATGCGACCTGTAATCTCA 184
                  CTTTCAAAGGGCCAGGATACCCAACTTGGAATGCTGTTTTGGGTTGGTCCTTAGATGGTA 175
                                                                                                                                                                                                                  236 CTTCACAAACATCTGTTGATTTAACTGCCGATGGTGTTAAATATGCTACTTGTCAATTTT 295
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                                                                                                                                              363 CATACCAAGGICCACAAATICCIACCIGGACIGCAGAACIAACAIGGITITIGAAIGGAG 304
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735 bp DNA linear GSS 21-MAY-2000 nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
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Tetraodon nigroviridis.
Tetracodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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Direct Submission
Submitted (12-APR-2000)
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/rote="Genoscope sequence ID : COBG123AG03LP1-end : T7"
//rote="Genoscope sequence ID : COBG123AG03LP1-end : T7"
45 c 223 g 197 t 28 others
                   Bouneau, L., Fisher, C.
                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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nigroviridis
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Bost-Chilus,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                              Human gene number estimate provided by genome wide analysis
Tetraodon nigroviridis DNA sequence
1 (bases 1 to 735)
cost.crollius.H., Jaillon,O., Dasilva,C., Bouneau,L., Fish
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="123M05"
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Pred. No. 3.8e-15;
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CNSOlVTG 773 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 199C24 of library G from Tetraodon nigroviridis, genomic survey
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/clone="199C24"
/clone_lib="G"
/note="Genoscope sequence ID : COAG199BB12LP1-end : T7"
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                                                                                                                                                                                          1613 TCAGAGAACCTCCAAACCCAACTGTCACCACCACT 1647
                                                                                                                                                                                                                                                                          CTACTACTACTACTACTACTACTACTACTGCT 13
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AL165549.1 GI:7807606
GSS; genome survey sequence.
Tetraodon nigroviridis.
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CNSOlXFI 1762 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 202124 of library G from Tetraodon nigroviridis, genomic survey
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1 (bases 1 to 762)

1 (bases 1 to 763)

2 (bases 1 to 762)

3 (bases 1 to 763)

Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1836 GCCACCAAACCACACTGTCACTACTACTGAGTATTGGTCTCAATCGTTTGCTACTACCAC 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1896 AACTGTAACTGGTCCACCAAGTGGCACTGATACTGTTATCATTAGGGAACCAAACCC 1955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CACTGAAGAATGGGTTGGGACTTATGGTAGTGTCGTTACGCAACTGGAATTACCTGGAGG 348
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                                                                                                                                                                                                                                                                                                   /note="similar to 074623 [ Agglutinin-like protein 3 precursor, ALS3 ] [ Candida albicans]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 GCCACCGAATCCTACCATCACGACAATTTTGGGGTCAAGTATTTCACTACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AACTTACAAGAATAGTGCAAATAGTGTTGATACTGTTGTGATTTATGCTCCTGTCAAATCC
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  sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98.4; DB 17
Pred. No. 3.7e-14;

    908
    /organism="Candida tropicalis"

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                            the other extremity of this insert. Location/Qualifiers
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     keywords for description of this
                                                                                                                                                          /db_xxref="taxon:5482"
/clone="BDOAA013B05"
/clone_11b="BDOAA"
/note="end : T7"
<47. .>727
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                                                                                                                                      /strain-"CBS 94"
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                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSO7DJI 908 bp DNA linear GSS 08-JUL-2001
T7 end of clone BD0AA013B05 of library BD0AA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Soudet,J.L., Adjele,M., Artiquenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvedlise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P., and Weissenbach,J.
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FEBS Lett. 487 (1), 3-12 (2000)
                                                  1319 CTACTGAATATTGGTCTCACACCTACAACCACTACAGTTACTGCTCCTCCAGGTG 1378
                                                                                                                                                                                                                                                                    1439 GGTCACAATCCTTTGCTACTACTACTGCTGTTACTGCTCCTCCAGGTGGTACTGACTCAG 1498
                                                                                                                                                                                                                                                                                                                                                                         1499 TAATTATCAGAGAACCACCAAATCCAACTGTCACTACAACCGAGTATTGGTCTCAATCCT 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGCTACTACTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAG 1618
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                                                                                                                                                          1379 GTACCGATACTGTGATTATCAGAGCCACCAAACCATACTGTCACTACTACTGAATATT 1438
352 CTACTACTACTGCAWACCAGCATACATACTACTGCTACTACTACATGCTACATACTGCAA 411
                                                                                                       412 CTACWGCAACTGCWACTRCTACAGCWACTACTACCACWACAACAACTACWRCWRCAAA 471
                                                                                                                                                                                                               472 CTACTGCTACAACTACTACTRCWACTGCTACTACTACTACTACTACTACTACTA 531
                                                                                                                                                                                                                                                                                                                         532 CTACTACWGCTACWACTACWGCTACTACTGCTACTRCAACTGCTACTACWACTGCTACWA 591
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AL440548.1 GI:12223959
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                                           Genoscope.

Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as ascale chone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cos.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                           Length 762
                                                                                                                                                                                                                                                                            6 others
pufferfish Tetraodon nigroviridis
                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="202124"
/clone="lbb="Ganscope sequence ID : COAC
/note="Genoscope sequence ID : COAC
/note="Genoscope sequence ID : COAC
                                                                                                                                                                                                                                                                                                                        Score 97; DB 17; I
Pred. No. 7.7e-14;
3; Mismatches 356;
                                                                                                                                                               Location/Qualifiers
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Matches 308;
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                            REFERENCE
AUTHORS
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AZ185454 1005_AZ_H08_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone plate=1005 Col=16 Row=O, DNA sequence.
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Cameron, R. A. Mahairas, G., Rast, J. P., Martinez, P., Biondi, T. R., Swartzell, S., Wallace, J. C., Poustka, A. J., Livingston, B. T., Wray, G. A., Ettensohn, C. A., Lehrach, H., Britten, R. J., Davidson, E. H. an Hood, L.
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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in B
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000) 20402566
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/db_xref="taxon:7668"
/clone="Plate=1005 Col=16 Row=0"
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Pred. No. 3e-13;
0; Mismatches 262;
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California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                             Strongylocentrotus purpuratus. Strongylocentrotus purpuratus
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High quality sequence stop: 8
Location/Qualifiers
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Plate: 1005 row: O column
Seq primer: T7
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Fax: (626) 793-3047
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Best Local Similarity 50.0
Matches 263; Conservative
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AUTHORS
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AUTHORS
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1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:
Lobela_Pedamp.mrc.ac.uk
Vector: pBluescript II KS
V_Lype: phagemid
1486 GGTACTGACTCAGTAATTATCAGAGAACCACCAAATCCAACTGTCACTACAACCGAGTAT 1545
                                                            1546 TGGTCTCAATCCTTTGCTACTACTACTACTACTGCTCCTCCAGGTGGTACTGACTCA 1605
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                                                                                                                                                                                                                                    FR0048173 501 bp DNA linear GSS 05~,
Fugu rubripes GSS sequence, clone 264E22cA9, genomic survey
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                                                                                                                          GTAATTATCAGAGAACCTCCAAACCCAACTGTCACCACCACTGAAT 1651
                                                                                                                                                       ACTACTAACGAGTAACGAGTAAGTATTTTTCATCAACAATAATT
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Pred. No. 1.7e-12;
0; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //organism="Takifugu rubripes"
/db_xref="taxon.31033"
/clone="264E22cA9"
/clone_1ib="BAC_264E22"
161 c 35 g 173 t
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Takifugu rubripes:
Takifugu rubripes
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AL444958.1 GI:12053458
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The BACs can be
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es 236; Conserv
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FR0048173
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CNS02HA4 1989 bp DNA linear GSS 13-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 139021 of library G from Tetraodon nigroviridis, genomic survey
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nigroviridis
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Tetracodon infgroviridis.

Tetracodon infgroviridis.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetracodontiformes;

Tetracodontidae; Tetracodon:

(bases 1 to 989)

Rosst-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F.,

Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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41 others
1423 ACTACTACTGAATATTGGTCACAATCCTTTGCTACTACTACTGTTACTGTTGCTCCTCCT 1482
                                                                                                    1483 GGTGGTACTGACTCAGTAATTATCAGAGAACCACCAAATCCAACTGTCACTACAACCGAG 1542
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Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                ACTACTGCTGCTACTACTACTACTACTACTAGTAGTAGTACTACTACTAGTAGTAGT
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/db_xref="taxon:99883"
/clone="139021"
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9; Mismatches 259;
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/note="Genoscope
245 c 122
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ilarity 47.0%;
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Genoscope.
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238; Conserv
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1162 ACAGCTACTGTTATTGTTGATGTGCCATATCATACTACCACACACTGTTACCAGTGAATGG 1221
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GSS; genome survey sequence.
GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 ISB. UK Email:
biohelp@hgmp.mrc.ac.uk
 CAAGTTTGAAACCAAGTATGGGTGAAAATTCTGGATTAACTACTTCTACTGAAATTGAAG 3292
                                                      CTACAACAACCAGTCCTACAGAAGCTCCATCACCTGCTGTTTCTTCTGGTACTGATGTAA 3352
                                                                                                            CTACTGAACCAACTGATACTAGAGAACAACCTACTACATATCAACTACTTCAAAAACAA 3412
                                                                                                                                                                 3413 ACAGTGAACTGGTTGCTACTACAAGCTACTAATGAAAATGGTGGTAAATCTCCATCAA 3472
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Fugu rubripes GSS sequence, clone 263KL5bD8, genomic survey
sequence.
                 CTGATTTAACATCAAGCTTGACAACAGGCACCTCAGCATCTACAAGTGCTAATAGCGAAC
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The BACs can be obtained from http://www.incyte.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Takifugu rubripes"
/db xref="taxon:31033"
/clone="263x15bbB"
/clone_11b="BAC 263x15"
163 c 45 g 158 t
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                                                                                                                                                                                                                                                                                                                                                511 ATAATAATAMTACTACTCCTCCATC 536
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                                 1222 ACAGGAACAATCACTACCACCACAACTCGTACCAATCCAACTGATTCAATTGACACAGTG 1281
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Pred. No. 3.1e-10;
0; Mismatches 214; Indels
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/db_xref="taxon:31033"
/clone="154E17aC12"
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140 c 64 g 144
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Takifugu rubripes.
Takifugu rubripes
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al Similarity 49.3%;
208; Conservative (
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Clark.M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by Preshington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                        329 GCTACTACTGCTGCTGCTACTACTACTACTACTGCTGCTGCTGCTACTACTACT
                                       1336 CAGTCCTTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGTACCGATACTGTGATT
                                                         1456 ACTACTACTGCTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAACCA
29 ACTGGAGACNTCAAATAACCTCAGTGGCCTCTAACTCCTACTAATGCTACTACTACTACT
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"Da_xref="taxon:7955"
/clone="5412044"
/clone_lib="Sugano SJD adult male"
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WashU Zebrafish EST Project 1998
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/ueb_bost="DH108" (phage resistant)"
/lab_host="DH108" (phage resistant)"
/note="Vector: pME18S-FL3: Site_1: DraIII (CACCATGTG);
Site_2: DraIII (CACTGTGTG); lst strand CDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTT];
double-stranded CDNA was ligated to a DraIII adaptor [TGTTGGCTTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 wector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer CATCTGCTCTAAAACTGCG and 3' end primer
CGACCTGCAACTGGAGGAR."
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Job time: 3377 secs
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